

FIG S1 Neighbor-joining tree constructed with *recA* (a), *atpD* (b), *dnaK* (c), *glnII* (d), *gryB* (e), *rpoB* (f) gene sequences showing the phylogenetic relationships of the rhizobial populations isolated from the different land-use and crop managements. Accession numbers of the sequences in GenBank database presented in parentheses strains are those used in this study. Bootstrap values only higher than 50 were shown at nodes. Scale bars represent 0.5% or 1% of nucleotide substitutions.

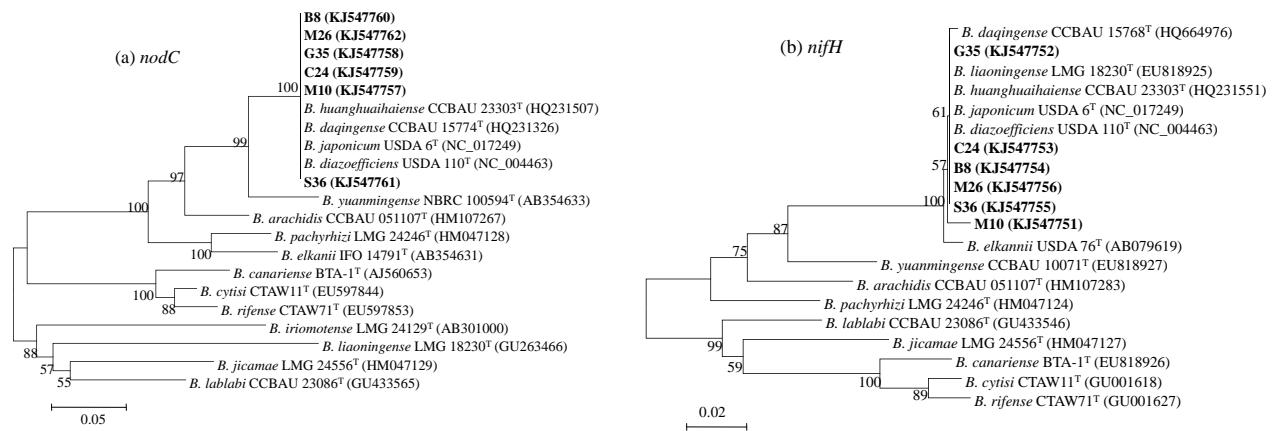


FIG S2 Neighbor-joining tree constructed with *nodC* (a) and *nifH* (b) gene sequences showing the phylogenetic relationships of the rhizobial populations isolated from the different land-use and crop managements. Bootstrap values only higher than 50 were shown at nodes. Accession numbers of the sequences in GenBank database presented in parentheses strains are those used in this study. Scale bars represent 2% or 5% of nucleotide substitutions.

TABLE S1 Similarities of the housekeeping gene sequences between the new isolates and the reference strains.

Representative isolate [#]	Phylogenetic affiliation*							Definition of genospecies
	<i>recA</i>	<i>atpD</i>	<i>glnII</i>	<i>gryB</i>	<i>rpoB</i>	<i>dnaK</i>	MLSA	
M10	97.3%	98.6%	97.6%	95.8%	98.1%	97.3%	97.7%	<i>B. sp. I</i>
B8, C24	99.1-99.8%	100% (B8)/ <i>B. diazoefficiens</i> USDA 110 96.3% (C24)	98.0-99.2%	98.1%	98.1-99.5%	98.2-98.6%	98.3-98.8%`	<i>B. japonicum</i>
G35	95.7%	<i>B. diazoefficiens</i> USDA 110 96.3%	97.4%	<i>B. diazoefficiens</i> USDA 110 95.3%	98.0%	<i>B. huanghuaihaiense</i> CCBAU 23303 ^T 97.3%	96.3%	<i>B. sp. II</i>
S36, M26	<i>B. arachidis</i> CCBAU 051107 ^T 95.2-95.4%	<i>B. diazoefficiens</i> USDA 110 94.6-96.3%	<i>B. diazoefficiens</i> USDA 110 96.4-98.2%	<i>B. diazoefficiens</i> USDA 110 96.0%	<i>B. arachidis</i> CCBAU 051107 ^T 96.1-96.5%	<i>B. huanghuaihaiense</i> CCBAU 23303 ^T 97.3-97.7%	<i>B. diazoefficiens</i> USDA 110 95.5%	<i>B. sp. III</i>

*All the similarities were compared with *B. japonicum* USDA 6^T, except specially indicated.

M10 had the same *recA* gene sequence to G1, G8, G9, G10, G11, G12, G13, G14, G17, G19, G20, G22, G24, G25, G26, G30, G31, B1, B2, B3, B4, B5, B6, C1, C2, C3, C4, C5, C6, C7, C8, C9, C10, C11, C12, C13, C14, C15, C16, C17, C18, C19, C20, S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S26, S27, S28, S29, S30, S31, S32, S33, S34, S35, M1, M2, M3, M4, M5, M6, M7, M8, M9, M11, M12, M13, W1, W2, W3, W4, W5, W6, W7, W8, W9, W10, W11, W12, W13, W14, W15, R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R13, R14, R15, R16, R17, R18, R19, R20, R21, R22, R23, R24, R25, R26;

G35 had the same *recA* gene sequence to strains of G21, G27, G29;

B8 had the same *recA* gene sequence to strains of G33, G34, G36, G37, G40, B7, B9; C21, C22, C23;

C24 had the same *recA* gene sequence to strains of R27, R28, R29, R30, R31, R32, R33, R34, R35, R36;

S36 had the same *recA* gene sequence to strains of G2, G3, G4, G5, G6, G7, G15, G16, G18, G23, G28, G32, G38, G39, B10, B11, B12, B13, B14, B15, B16, B17, B18, B19, B20, B21, B22, B23, B24, B25, B26, B27, B28, B29, B30, B31, B32, B33, B34, B35, B36, B37, B38, B39, B40, C25, C26, C27, C28, C29, C30, C31, C32, C33, C34, C35, G36, C37, C38, C39, C40, , S37, S38, S39, S40; R37, R38, R39, R40

M26 had the same *recA* gene sequence to strains of M14, M15, M16, M17, M18, M19, M20, M21, M22, M23, M24, M25, M27, M28, M29, M30, M31, M32, M33, M34, M35, M36, M37, M38, M39, M40, W16, W17, W18, W19, W20, W21, W22, W23, W24, W25, W26, W27, W28, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40.

TABLE S2 The number, ratio and percentage of the isolates in genospecies and in the sampling sites.

Isolate*	Distribution†
<i>Bradyrhizobium</i> sp. I (132/280, 47.1%)	
G1, G8, G9, G10, G11, G12, G13, G14, G17, G19, G20, G22, G24, G25, G26, G30, G31, B1, B2, B3, B4, B5, B6, C1, C2, C3, C4, C5, C6, C7, C8, C9, C10, C11, C12, C13, C14, C15, C16, C17, C18, C19, C20, S1, S2, S3, S4, S5, S6, S7, S8, S9, S10, S11, S12, S13, S14, S15, S16, S17, S18, S19, S20, S21, S22, S23, S24, S25, S26, S27, S28, S29, S30, S31, S32, S33, S34, S35, M1, M2, M3, M4, M5, M6, M7, M8, M9, M10 , M11, M12, M13, W1, W2, W3, W4, W5, W6, W7, W8, W9, W10, W11, W12, W13, W14, W15, R1, R2, R3, R4, R5, R6, R7, R8, R9, R10, R11, R12, R13, R14, R15, R16, R17, R18, R19, R20, R21, R22, R23, R24, R25, R26	GL (17) BL (6) CL (20) S-S (35) M-M (13) W-W (15) M/S/W (26)
<i>B. japonicum</i> USDA6 ^T (22/280, 7.8%)	GL (5), BL (3), CL (4), M/S/W (10)
G33, G34, G36, G37, G40, B7, B8 , B9, C21, C22, C23, C24 , R27, R28, R29, R30, R31, R32, R33, R34, R35, R36	
<i>Bradyrhizobium</i> sp. II (4/280, 1.4%)	GL (4)
G21, G27, G29, G35	
<i>Bradyrhizobium</i> sp. III (122/280, 43.6%)	
G2, G3, G4, G5, G6, G7, G15, G16, G18, G23, G28, G32, G38, G39, B10, B11, B12, B13, B14, B15, B16, B17, B18, B19, B20, B21, B22, B23, B24, B25, B26, B27, B28, B29, B30, B31, B32, B33, B34, B35, B36, B37, B38, B39, B40, C25, C26, C27, C28, C29, C30, C31, C32, C33, C34, C35, G36, C37, C38, C39, C40, S36 , S37, S38, S39, S40, M14, M15, M16, M17, M18, M19, M20, M21, M22, M23, M24, M25, M26 , M27, M28, M29, M30, M31, M32, M33, M34, M35, M36, M37, M38, M39, M40, W16, W17, W18, W19, W20, W21, W22, W23, W24, W25, W26, W27, W28, W29, W30, W31, W32, W33, W34, W35, W36, W37, W38, W39, W40, R37, R38, R39, R40	GL (14) BL (31) CL (16) S-S (5) M-M (27) W-W (25) M/S/W (4)

*. Contents in brackets are the isolate number/total, percentage.

†. Numbers in brackets are the isolate number in each cultivation management. GL, grassland since 1985; BL, bareland since 1985; CL, cropland with maize/soybean/wheat rotation without fertilizer supply since 1985; S-S, soybean monoculture since 1990; M-M, maize monoculture since 1990; W-W, wheat monoculture since 1990; M/S/W, maize/soybean/wheat rotation with chemical fertilizer supply since 1990.